



## BLASTP 2.2.1 [Apr-13-2001]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1003946835-11427-26633

### Query=

(10 letters)

CATDIKGATC circular

### Database: nr

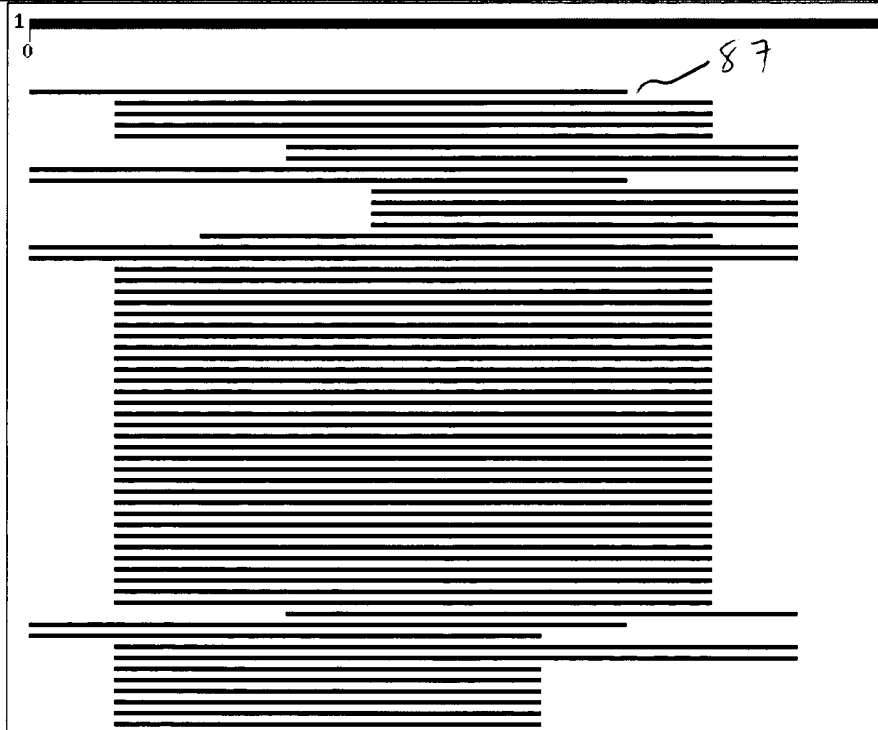
777,663 sequences; 247,121,334 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Score E

10 24/01 2:10 PM

gi 181643 gb AA00745.1	(U58941) pilin [Neisseria gonorrh...	21	1058
gi 44161 gb AA00245.1	(AF042049) beta-1,4-xylosidase [L...	21	1058
gi 44641 gb AA00142.1	(U28940) pilin [Neisseria gonorrh...	21	1058
gi 44641 gb AA00143.1	(U28940) pilin [Neisseria gonorrh...	21	1058
gi 113117 gb AA00764.1	(U58941) pilin [Neisseria gonorrh...	21	1058
gi 10431 pir S1360	nerve growth factor - monocled cobra ...	21	1058
gi 28101 gb AA00014.1 AF173151	(AF273153) selenophosph...	21	1058
gi 44641 gb AA00142.1	(U28940) pilin [Neisseria gonorrh...	21	1058
gi 113117 sp P21177	NGF NERVE GROWTH FACTOR (NGF)	21	1058
gi 113117 gb AA00744.1	(U58940) pilin [Neisseria gonorrh...	21	1058
gi 113117 sp P21178	NGF BDNF NERVE GROWTH FACTOR RECEPTOR...	21	1058
gi 113117 pir A5418	nerve growth factor beta chain prec...	21	1058
gi 113117 gb AA00743.1	(AF314084) envelope glycoprotein...	21	1058
gi 113117 emb W00446.1	A01160f) membrane tyrosine pho...	21	1058
gi 180023 gb AA00484.1	(M16023) gonococcal pilin protein ...	21	1058
gi 1473281 ref NP_001556.2	hypothetical protein XP_001556...	21	1058
gi 1801346 gb AA00743.1 AF364214	(AF364229) ORF154 [w...	21	1058
gi 180023 emb CAB4336.2	(A0178063) selenophosphate synt...	21	1058
gi 44161 gb AA00245.1	(AF042049) beta-1,4-xylosidase [L...	21	1058
gi 1801346 ref NP_001060.1	Glycerol-3-P dehydrogenase [Ch...	21	1058
gi 1801346 ref NP_001060.1	beta-1,4-xylosidase (EC 3.2.1.1)...	21	1058
gi 113117 gb AA00743.1	(AF314084) pilus subunit [Neisser...	21	1058
gi 113117 ref NP_001060.1	hypothetical protein FL133078 [...	21	1058
gi 113117 gb AA00743.1	(AF314084) pilus subunit [Neisser...	21	1058
gi 113117 gb AA00743.1	(U58943) pilin [Neisseria gonorrh...	21	1058
gi 113117 gb AA00743.1	(AF314084) pilus subunit [Neisser...	21	1058
gi 1801346 ref NP_001060.1	quinone oxidoreductase [Bacill...	21	1058
gi 1801346 pir S1360	nerve growth factor - Naja naja xgi7...	21	1058
gi 113117 gb AA00743.1	(U58941) pilin [Neisseria gonorrh...	21	1058
gi 113117 sp P21177	NGF NERVE GROWTH FACTOR (NGF)	21	1058
gi 1801346 ref NP_001060.1	putative beta-galactosidase [A...	21	1470
gi 1801346 ref NP_001060.1	L-ASPARAGINASE (L-ASPARAGINE...	21	1470
gi 1801346 gb AA00743.1 AF169653	(AF169653) 20S proteaso...	21	1470
gi 1801346 pir S1360	potassium channel protein Slo - fruit...	21	1470
gi 1801346 ref NP_001060.1	unknown protein [Arabidopsis t...	21	1470
gi 1801346 pir A1590	calcium-activated potassium channel, ...	21	1470
gi 1801346 emb W00446.1	A01160f) transcription factor ...	21	1470

## Alignments

cg141421.gb|AV027324.1| (U30306) T-cell receptor alpha V-J junction [Homo sapiens]  
Length: 16

Score = 23.5 bits (4%), Expect = 161  
Identities = 7/3 (67%), Positives = 7/3 (83%)

```

Query: 1 CATDIXGA 5
      CATDI  GA
Skip: 2 CATDITGA 4

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gi114339444|emb|CAC4518.11 (A/E14790) putative zinc finger protein [Homo sapiens]  
length = 167

Score = 21.7 bits (46%), Expect = 326  
Identities = 6/7 (85%), Positives = 6/7 (85%)

```

Query: 4      DINGLET 10
          DING ET
Shift: 49'    DINGLET 500

```

cd1\_442303\_gblnAF164\_5.1 AF164358) outer surface protein C precursor [Morrelia sp.  
length = 31.

Score = 31.7 bits (46%), Expect = 32  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAE 9  
 ATDIKGAE  
 Subject: 164 ATDIKGAE 171

Date

gi|128165|sp|P.9675|NGF PRANA BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)  
 Length = 241

Score = 22.7 bits (46), Expect = 326  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDIKGAE 4  
 ATDIKGAE  
 Subject: 144 ATDIKGAE 186

gi|69054|pir||NGFRA nerve growth factor beta chain precursor - multimammate rat  
 (Mastomys natalensis)  
gi|202116|gb|AA40849.1| (M22743) nerve growth factor [Mastomys natalensis]  
 Length = 303

Score = 22.7 bits (46), Expect = 326  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDIKGAE 4  
 ATDIKGAE  
 Subject: 111 ATDIKGAE 118

gi|14712326|ref|XP\_044985.1| hypothetical protein XP\_044985 [Homo sapiens]  
 Length = 606

Score = 22.7 bits (46), Expect = 326  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 4 DIKGAE 19  
 DIKGAE  
 Subject: 119 DIKGAE 5.1

gi|15608303|ref|NP\_47159.1| SSU ribosomal protein S11P (rpsK) [Methanococcus janna  
gi|1710719|sp|P54021|RS11 METUA 30S RIBOSOMAL PROTEIN S11P  
gi|111901|pir|H64503|ribosomal protein S11 - Methanococcus jannaschii  
gi|1599936|gb|AA33171.1| (U67475) SSU ribosomal protein S11P (rpsK) [Methanococcus  
jannaschii]  
 Length = 119

Score = 22.7 bits (46), Expect = 326  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDIKGAE 9  
 ATDIKGAE  
 Subject: 25 ATDIKGAE 32

gi|16123334|ref|NP\_406647.1| 4-methyl-5(B-hydroxyethyl)-thiazol monophosphate biosy  
enzyme [Yersinia pestis]  
gi|1594111|ref|AAC33407.1| (AJ41415) 4-methyl-5(B-hydroxyethyl)-thiazol monophosp  
biosynthesis enzyme [Yersinia pestis]  
 Length = 196

Score = 22.3 bits (45), Expect = 438  
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 1 IKGAET 10  
 IKGAET  
 Subject: 76 IKGAET 81

Date

gi|15800174|ref|NP\_286166.1| 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate s

[Escherichia coli O157:H7 EDL933]  
gi|15829732|ref|NP\_303515.1| 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate s  
[Escherichia coli O157:H7]  
gi|12513290|gb|AA654774.1|AF005221.1| AE005221| 4-methyl-5(beta-hydroxyethyl)-thia  
synthesis [Escherichia coli O157:H7 EDL933]  
gi|13359459|bj|BA633901.1| (AP002551| 4-methyl-5(beta-hydroxyethyl)-thiazole monop  
synthesis [Escherichia coli O157:H7]  
Length = 196

Score = 21.3 bits (45), Expect = 43e-  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 1 IKGAEC 11

IKGAEC

Subject: 78 IKGAEC 88

>gi|7527613|pir|T37201 Notch homolog protein - sea squirt (Halocynthia roretzi)  
gi|3940867|gb|BAAC5571.1| (AB001327) HsNotch protein [Halocynthia roretzi]  
Length = 2352

Score = 21.3 bits (45), Expect = 43e-  
Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 2/10 (20%)

Query: 1 CATIKGAEC 10

CATIK EC

Subject: 991 CATIK--EC 796

>gi|6680641|sp|Q46248|THI1 ECOLI 4-METHYL-5(B-HYDROXYETHYL)-THIAZOLE MONOPHOSPHATE B  
ENZYME  
Length = 196

Score = 21.3 bits (45), Expect = 43e-  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 5 IKGAEC 10

IKGAEC

Subject: 76 IKGAEC 81

>gi|16128409|ref|NP\_414268.1| 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate s  
[Escherichia coli K12]  
gi|7429595|pir|H64771 hydroxymethylpyrimidine kinase (EC 2.7.1.49) - Escherichia c  
gi|1100871|gb|AAAE7734.1| (U34903) ThiC [Escherichia coli]  
gi|1773183|gb|JAB40180.1| (U80664) 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphat  
biosynthesis protein [Escherichia coli]  
gi|1780616|gb|AAC73527.1| (AE000148) 4-methyl-5(beta-hydroxyethyl)-thiazole monopho  
synthesis [Escherichia coli K12]  
Length = 196

Score = 21.3 bits (45), Expect = 43e-  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 5 IKGAEC 10

IKGAEC

Subject: 78 IKGAEC 83

>gi|1242611|cds|1HE0\_B Chain B, Molecular Structure Of A High Potential Cytochrome C  
Isolated From Rhodopila Globiformis  
gi|1242611|cds|1HE0\_A Chain A, Molecular Structure Of A High Potential Cytochrome C  
Isolated From Rhodopila Globiformis  
Length = 106

Score = 21.3 bits (45), Expect = 43e-  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 CATIKGA 8

C TDIKGA

Sbjct: 22 CHTDIKGA 29

gi|14588553|gb|AAK01629.1| (AY037148) phosphatidylethanolamine binding protein [Hem  
Length = 117

Score = 21.8 bits (44), Expect = 588  
 Identities = 6/7 (86%), Positives = 7/7 (99%)

Query: 3 TDIKGAE 9  
 TDIKGA+  
 Sbjct: 116 TDIKGAD 122

gi|15014803|gb|AAH11123.1|AAH11123 (58011123) Similar to nerve growth factor, beta  
Length = 124

Score = 21.4 bits (43), Expect = 712  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDIKGAE 4  
 ATDIKG E  
 Sbjct: 215 ATDIKGKE 122

gi|2305312|ref|NP\_035637.1| nerve growth factor, beta [Mus musculus]  
gi|69053|pir|INSMMSG nerve growth factor beta chain precursor - mouse  
gi|55305|emb|CAAG411.1| (V00936) precursor of NGF [Mus musculus]  
gi|500684|gb|AAA39511.1| (M14805) nerve growth factor beta [Mus musculus]  
gi|337171|gb|AAA37646.1| (M17398) nerve growth factor [Mus musculus]  
gi|337444|gb|AAA38115.1| (M35773) nerve growth factor [Mus musculus]  
gi|337444|gb|AAA39511.1| (F01719) prepro-beta-nerve growth factor [Mus musculus]  
gi|467511|gb|AAA37847.1| (M17106) nerve growth factor [Mus musculus]  
gi|233610|prf|1387134A nerve growth factor precursor [Mus musculus]  
Length = 127

Score = 21.4 bits (43), Expect = 784  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAE 9  
 ATDIKG E  
 Sbjct: 215 ATDIKGKE 122

gi|69051|pir|INSHUBM nerve growth factor beta chain precursor - human (fragment)  
gi|23053|prf|1387134A nerve growth factor beta [Homo sapiens]  
Length = 126

Score = 21.4 bits (43), Expect = 784  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDIKGAE 4  
 ATDIKG E  
 Sbjct: 194 ATDIKGKE 201

gi|112441|gb|AA48444.1| (M26810) nerve growth factor [Gallus gallus]  
Length = 113

Score = 21.4 bits (43), Expect = 784  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 3 ATDIKGAE 9  
 ATDIKG E  
 Sbjct: 32 ATDIKGKE 39

gi|34671|pir|A2631 nerve growth factor beta chain precursor - bovine (fragment)  
gi|163410|gb|AAA30686.1| (M26809) nerve growth factor [Bos taurus]  
Length = 125

Score = 21.4 bits (43), Expect = 7e-9  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGA E  
 ATDIK E  
 Sbjct: 33 ATDIKKE 40

gi|4248742|gb|AA0266.3.2| (-S62039) nerve growth factor [Mus sp.]  
 Length = 171

Score = 21.4 bits (43), Expect = 7e-9  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 3 ATDIKGA E  
 ATDIK E  
 Sbjct: 149 ATDIKKE 156

gi|1115531|pir|I58570 beta-nerve growth factor - rat (fragment)  
gi|356623|gb|AA4169.1| (M36589) beta-nerve growth factor [Rattus norvegicus]  
 Length = 148

Score = 21.4 bits (43), Expect = 7e-9  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 4 ATDIKGA E  
 ATDIK E  
 Sbjct: 153 ATDIKKE 160

gi|4306391|ref|NP\_01497.1| nerve growth factor, beta polypeptide; Nerve growth fac  
[Homo sapiens]  
gi|128161|sp|P01138|NGF HUMAN BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)  
gi|124477|emb|C7A36832.1| (X52599) beta nerve growth factor (AA 1-241) [Homo sapiens]  
gi|119303|gb|AA59951.1| (M21961) nerve growth factor beta [Homo sapiens]  
gi|67198|emb|CAA24735.1| (V01511) beta-nerve growth factor [Homo sapiens]  
 Length = 141

Score = 21.4 bits (43), Expect = 7e-9  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 5 ATDIKGA E  
 ATDIK E  
 Sbjct: 149 ATDIKKE 156

gi|35417.4|sp|P13690|NGF BOVIN BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)  
gi|138-7|0|emb|CAAF059.1| (Y09566) beta-nerve growth factor [Bos taurus]  
 Length = 231

Score = 21.4 bits (43), Expect = 7e-9  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 6 ATDIKGA E  
 ATDIK E  
 Sbjct: 139 ATDIKKE 146

gi|331616|pdb|1SGFY|Chain Y, Crystal Structure Of 7s Ngf: A Complex Of Nerve Grow  
Factor With Four Binding Proteins (Serine Proteinases)  
gi|331616|5|pdb|1SGFB|Chain B, Crystal Structure Of 7s Ngf: A Complex Of Nerve Grow  
Factor With Four Binding Proteins (Serine Proteinases)  
 Length = 116

Score = 21.4 bits (43), Expect = 7e-9  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 7 ATDIKGA E

ATDING E  
 Subject: 28 ATDINGKE 35

gi|4034770|sp|P21617|NGF\_XENLA NERVE GROWTH FACTOR PRECURSOR (NGF)  
 Length = 131

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGAE 9  
 ATDING E  
 Subject: 141 ATDINGKE 143

gi|1351445|sp|F15473|NGF\_RAT BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)  
 Length = 131

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGAE 9  
 ATDING E  
 Subject: 149 ATDINGKE 155

gi|128150|sp|EC5000|NGF\_CHICK BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)  
 Length = 145

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGAE 9  
 ATDING E  
 Subject: 151 ATDINGKE 159

gi|1361674|ref|XP\_002122.2| nerve growth factor, beta polypeptide [Homo sapiens]  
gi|16150835|ref|XP\_024005.1| hypothetical protein XP\_058005 [Homo sapiens]  
gi|5917605|gb|AA054475.1|AF150960.1 (AF150960) nerve growth factor B [Homo sapiens]  
gi|7018400|emb|CAB24625.1| (AL049325) dJ662B22.1 (nerve growth factor, beta polypep  
 sapiens)  
 Length = 141

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGAE 9  
 ATDING E  
 Subject: 149 ATDINGKE 156

gi|6815227|dbj|BAAN448.1 (AB037518) beta-nerve growth factor [Pan troglodytes]  
 Length = 141

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGAE 9  
 ATDING E  
 Subject: 142 ATDINGKE 156

gi|15611475|ref|NP\_223326.1| CHORISMATE SYNTHASE [Helicobacter pylori J99]  
gi|11151448|sp|Q6ZLR1|AROC\_HELPJ CHORISMATE SYNTHASE (5-ENOLPYRUVYLSHIKIMATE-3-PHOS  
 PHOSPHOLYASE)  
gi|743723|pir|F71911 chorismate synthase - Helicobacter pylori (strain J99)  
gi|4155160|gb|AA08159.1 (AE001492) CHORISMATE SYNTHASE [Helicobacter pylori J99]  
 Length = 565

Score = 21.4 bits (43), Expect = 789



Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 4 DIKGAEC 1  
DIKG EC  
Sbjct: 303 DIKGNED 315

gi|6815209|dbj|BAI40439.1| (AB037519) beta-nerve growth factor [Gorilla gorilla]  
Length = 151

Score = 11.4 bits (43), Expect = 789  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 5 ATDIKGAEC 9  
ATDIKG E  
Sbjct: 144 ATDIKKE 156

gi|14164981|gb|AAK55325.1|AF355457.1 (AF355457) thaumatin-like protein TLP7 [Hordeu  
Length = 157

Score = 11.4 bits (43), Expect = 789  
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 1 CATDI-KGAEC 10  
CATDI K EC  
Sbjct: 145 CATDITK--EC 153

gi|2490137|sp|Q29004 NGF PIG BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)  
gi|136548|pir|I45614 nerve growth factor B - pig (fragment)  
gi|833771|gb|AAK1401.1| (L31898) nerve growth factor B [Sus scrofa]  
Length = 155

Score = 11.4 bits (43), Expect = 789  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAEC 9  
ATDIKG E  
Sbjct: 137 ATDIKKE 144

gi|86383|pir||A26311 nerve growth factor beta chain precursor - chicken (fragment)  
gi|1334740|emb|CAAF7633.1 (X04003) prepro-polypeptide (aa -123 to 118); gtg start  
gallus]  
Length = 148

Score = 11.4 bits (43), Expect = 789  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAEC 9  
ATDIKG E  
Sbjct: 152 ATDIKKE 159

gi|8157159|gb|AAB3414.2| (S76884) truncated beta nerve growth factor; beta-NGF [Ho  
sapiens]  
Length = 157

Score = 11.4 bits (43), Expect = 789  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAEC 9  
ATDIKG E  
Sbjct: 28 ATDIKKE 35

gi|126161|sp|F11301 NGF MOUSE BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)  
Length = 151

Score = 11.4 bits (43), Expect = 789

Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAE 9  
ATDIKG E  
Sbjct: 149 ATDIKGKE 156

gi|127545|pcb|1WWW.W Chain W, Ngf In Complex With Domain 5 Of The Trka Receptor  
gi|127544|pcb|1WWW.V Chain V, Ngf In Complex With Domain 5 Of The Trka Receptor  
gi|108494|gb|AA73405.1| (M30504) nerve growth factor [synthetic construct]  
Length = 126

Score = 11.4 bits (43), Expect = 784  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAE 9  
ATDIKG E  
Sbjct: 28 ATDIKGKE 35

gi|6818711|db|BAAC0440.1| (AB037520) beta-nerve growth factor [Pongo pygmaeus]  
Length = 141

Score = 11.4 bits (43), Expect = 784  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAE 9  
ATDIKG E  
Sbjct: 149 ATDIKGKE 156

gi|122441|dbj|BAAD00008.1| (D00010) beta-nerve growth factor [Gallus gallus]  
gi|155704|emb|AA22783.1| (X04067) pro beta-nerve growth factor (aa 1-126) [Gallus  
Length = 126

Score = 11.4 bits (43), Expect = 784  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAE 9  
ATDIKG E  
Sbjct: 35 ATDIKGKE 41

gi|104144|pir|S14481 nerve growth factor beta chain precursor - African clawed frog  
gi|64919|emb|CAA39140.1| (X55716) nerve growth factor prepropeptide [Xenopus laevis]  
Length = 130

Score = 11.4 bits (43), Expect = 784  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAE 9  
ATDIKG E  
Sbjct: 149 ATDIKGKE 156

gi|2442172|pir|T04470 perml protein - barley (fragment)  
gi|2454692|gb|AA071670.1| (AF016327) Barperml [Hordeum vulgare]  
Length = 200

Score = 11.4 bits (43), Expect = 784  
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 1 CATDI-FGAEC 10  
CATDI F EC  
Sbjct: 123 CATDITY--EC 131

gi|126154|sp|P1909A|NGF CAVPO BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)  
gi|23006|pir|JL0007 nerve growth factor beta chain precursor - guinea pig  
Length = 241

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9  
 ATDING E  
 Sbjct: 14 ATDINGKE 156

gi|6315215|pdb|3AA90437.1| (AB037517) beta-nerve growth factor [Homo sapiens]  
 Length = 241

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9  
 ATDING E  
 Sbjct: 14 ATDINGKE 156

gi|6969512|gb|AAF33720.1|AF222682.1 (AF222682) beta nerve growth factor [Macaca fus  
 Length = 117

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9  
 ATDING E  
 Sbjct: 139 ATDINGKE 146

gi|1431713|pdb|1PTG A Chain A, Crystal Structure Of Beta Nerve Growth Factor At 2.5  
 Resolution In C2 Space Group With Zn Ions Bound  
gi|1431716|pdb|1PTG B Chain B, Crystal Structure Of Beta Nerve Growth Factor At 2.5  
 Resolution In C2 Space Group With Zn Ions Bound  
gi|1431717|pdb|1PTG C Chain C, Crystal Structure Of Beta Nerve Growth Factor At 2.5  
 Resolution In C2 Space Group With Zn Ions Bound  
 Length = 110

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9  
 ATDING E  
 Sbjct: 10 ATDINGKE 17

gi|656412|gb|AAFI235.1|AF145043.1 (AF145043) beta nerve growth factor [Cervus ela  
 Length = 87

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9  
 ATDING E  
 Sbjct: 12 ATDINGKE 19

gi|576004|pcb|1BET Beta-Nerve Growth Factor  
 Length = 107

Score = 21.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9  
 ATDING E  
 Sbjct: 19 ATDINGKE 16

gi|15705413|gb|AAL5874.1|AF411526.1 (AF411526) nerve growth factor beta [Homo sapi  
 Length = 241

Score = 11.4 bits (43), Expect = 789  
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 3 ATDINGAE 9  
 ATDING E  
 Subject: 140 ATDINGKE 156

gi|1291606|gb|AAFS2916.1| (AE003628) .ps2 gene product [Drosophila melanogaster]  
 Length = 515

Score = 11.0 bits (42), Expect = 105  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 CATDING 7  
 CAIDG G  
 Subject: 100 CAIDITG 216

gi|15793194|ref|NP\_253104.1| truncated pilin [Neisseria meningitidis Z2491]  
gi|11287672|pir|F83421 truncated pilin NMA0266 [imported] - Neisseria meningitidis  
 (group A strain Z2491)  
gi|1874014|emb|CAB63374.1| (AL162752) truncated pilin [Neisseria meningitidis Z2491]  
 Length = 141

Score = 21.0 bits (42), Expect = 105  
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 3 ATDING 7  
 ATDING  
 Subject: 14 ATDING 59

Database: nr

Posted date: Oct 23, 2001 6:02 PM

Number of letters in database: 247,121,334

Number of sequences in database: 777,863

Lambda	K	H
0.355	0.149	1.84

Gapped Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Hits to DB: 7,358,637

Number of Sequences: 777663

Number of extensions: 59715

Number of successful extensions: 1516

Number of sequences better than 20000.0: 1509

Number of HSP's better than 20000.0 without gapping: 1509

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1516

length of query: 10

length of database: 247,121,334

effective HSP length: 1

effective length of query: 9

effective length of database: 246,343,071

effective search space: 2217093039

effective search space used: 2217093039

T: 11

A: 40

X1: 14 (7.1 bits)

X2: 35 (14.6 bits)

X3: 58 (24.6 bits)  
S1: 33 (18.7 bits)  
S2: 33 (17.2 bits)